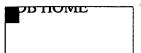
(sample of submitted file)



Structure Explorer - 1RYP



Title

Crystal Structure Of The 20S Proteasome From Yeast At 2.4 Angstroms Resolution

Classification

Multicatalytic Proteinase

Compound

Mol_Id: 1; Molecule: 20S Proteasome; Chain: A, B, C, D, E, F, G, H, I, J, K, L, M, N, O, P, Q, R, S, T, U, V, W, X, Y, Z, 1, 2; Ec: 3.4.99.46; Mutation: Chains H, V, T1A, Chain L, Z, K33R; Biological Unit: Yeast

Proteasome Seems To Be Composed Of 14 Different Subunits Which Form A Highly Ordered

Ring-Shaped Structure

REMARK

3

	Download/Display File
Summary Information	Save full entry to disk
View Structure	HEADER MULTICATALYTIC PROTEINASE 26-FEB-97 1RY TITLE CRYSTAL STRUCTURE OF THE 20S PROTEASOME FROM YEAST AT 2
Download/Display File	TITLE 2 ANGSTROMS RESOLUTION COMPND MOL_ID: 1; COMPND 2 MOLECULE: 20S PROTEASOME;
Structural Neighbors	COMPND 3 CHAIN: A, B, C, D, E, F, G, H, I, J, K, L, M, N, O, P, COMPND 4 R, S, T, U, V, W, X, Y, Z, 1, 2; COMPND 5 EC: 3.4.99.46;
Geometry	COMPND 6 MUTATION: CHAINS H, V, T1A, CHAIN L, Z, K33R; COMPND 7 BIOLOGICAL_UNIT: YEAST PROTEASOME SEEMS TO BE COMPOSEI COMPND 8 14 DIFFERENT SUBUNITS WHICH FORM A HIGHLY ORDERED
Other Sources	COMPND 9 RING-SHAPED STRUCTURE SOURCE MOL_ID: 1;
Sequence Détails	SOURCE 2 ORGANISM_SCIENTIFIC: SACCHAROMYCES CEREVISIAE; SOURCE 3 ORGANISM_COMMON: BAKER'S YEAST KEYWDS MULTICATALYTIC PROTEINASE, 20S PROTEASOME, PROTEIN
Explore	KEYWDS 2 DEGRADATION, ANTIGEN PROCESSING, HYDROLASE, PROTEASE EXPDTA X-RAY DIFFRACTION
SearchLite SearchFields	AUTHOR M.GROLL, L.DITZEL, J.LOEWE, D.STOCK, M.BOCHTLER, H.D.BARTUNI AUTHOR 2 R.HUBER REVDAT 1 15-APR-98 1RYP 0
	JRNL AUTH M.GROLL, L.DITZEL, J.LOWE, D.STOCK, M.BOCHTLER, JRNL AUTH 2 H.D.BARTUNIK, R.HUBER
	JRNL TITL STRUCTURE OF 20S PROTEASOME FROM YEAST AT 2.4 JRNL TITL 2 RESOLUTION JRNL REF NATURE V. 386 463 199
- /	JRNL REFN ASTM NATUAS UK ISSN 0028-0836 REMARK 1
	REMARK 2 REMARK 2 RESOLUTION. 1.9 ANGSTROMS.
9.5	REMARK 3 REFINEMENT. REMARK 3 PROGRAM : X-PLOR 3.1
	REMARK 3 AUTHORS : BRUNGER REMARK 3
	REMARK 3 DATA USED IN REFINEMENT. REMARK 3 RESOLUTION RANGE HIGH (ANGSTROMS): 1.9 REMARK 3 RESOLUTION RANGE LOW (ANGSTROMS): 50.
	REMARK 3 DATA CUTOFF (SIGMA(F)): 2. REMARK 3 DATA CUTOFF HIGH (ABS(F)): 100000000.
	REMARK 3 DATA CUTOFF LOW (ABS(F)): 0.1 REMARK 3 COMPLETENESS (WORKING+TEST) (%): 90.5 REMARK 3 NUMBER OF REFLECTIONS : 752101
	REMARK 3 REMARK 3 FIT TO DATA USED IN REFINEMENT.

CROSS-VALIDATION METHOD

: NULL